

Supplemental Information

Table S1. Statistics of *ACE2* gene in human populations of five continents.

Populations	SegSites ^a	θ ^a	π ^a	Tajima's D ^a	p ^a	Tajima's D ^b	p ^b
AFR	232	34.01	0.00046	-1.317	0.058	-1.328	0.082
AME	151	23.43	0.00034	-1.233	0.084	-1.264	0.097
EAS	147	21.52	0.00013	-2.233	<0.001	-2.268	0.002
EUR	133	19.44	0.00035	-0.754	0.285	-0.468	0.345
SAS	147	21.93	0.00033	-1.135	0.122	-1.025	0.156

^a represents the results that carried out by DNASP based on genetic variants.

^b represents the results that carried out by PopART based on haplotypes.

Table S2. Statistics derived from haplotypes of *ACE2* gene among populations.

Populations	π	SegSites	PSI	Tajima's D	p
ACB	0.1249	150	95	-1.188	0.118
ASW	0.1375	118	78	-1.159	0.125
ESN	0.1404	124	89	-0.951	0.179
GWD	0.1367	138	92	-0.891	0.197
LWK	0.1350	131	78	-0.948	0.180
MSL	0.1554	123	82	-0.736	0.246
YRI	0.1408	146	90	-0.840	0.213
CLM	0.2103	70	37	0.302	0.369
MXL	0.1372	71	36	-1.196	0.117
PEL	0.1212	83	41	-1.284	0.097
PUR	0.1731	88	44	-0.340	0.390
CDX	0.0925	68	41	-1.696	0.033
CHB	0.0883	58	27	-1.681	0.034
CHS	0.0799	49	11	-1.834	0.021
JPT	0.0910	51	25	-1.703	0.032
KHV	0.0730	70	27	-1.990	0.011
CEU	0.2329	62	37	0.663	0.252
FIN	0.2340	56	34	0.810	0.211
GBR	0.2276	61	35	0.501	0.302
IBS	0.2637	53	35	1.207	0.123
TSI	0.2720	50	34	1.353	0.098
BEB	0.1650	72	44	-0.550	0.311
GIH	0.2201	64	43	0.409	0.333
ITU	0.1867	70	42	-0.203	0.441
PJL	0.1955	75	41	0.014	0.475
STU	0.1519	72	50	-0.728	0.272

Statistics based on haplotypes were carried out by PopART. π represents nucleotide diversity. SegSites represents segregating sites. PSI represents parsimony-informative sites.

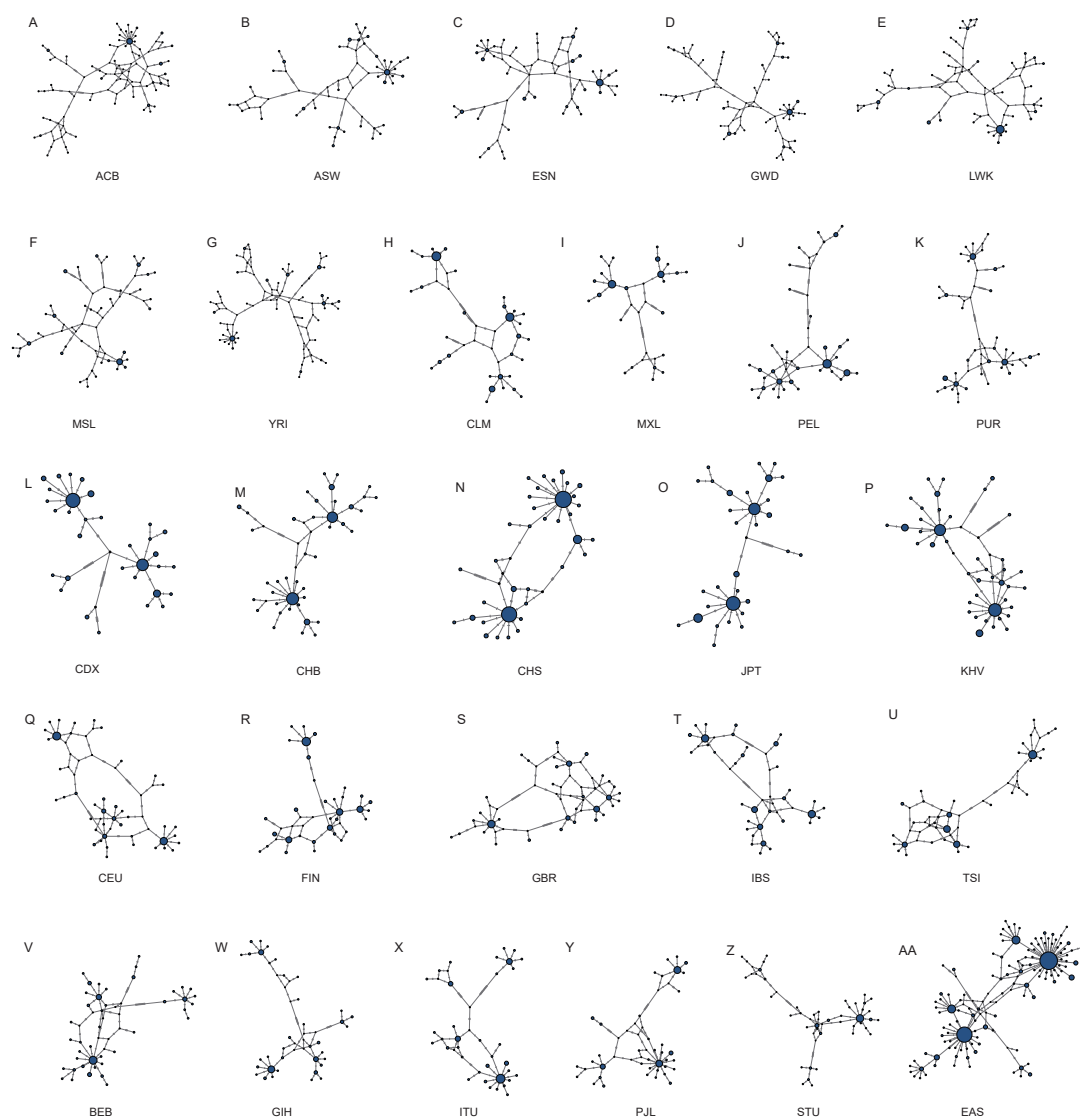


Figure S1. Integer neighbor joining networks derived from haplotypes of ACE2 in human populations. Haplotypes are represented by circles, and the size of the circle is proportional to the haplotype frequency. Short black vertical lines represent mutational steps. (A-G) belong to Africans. (H-K) belong to Americans. (L-P) belong to East Asians. (Q-U) belong to Europeans. (V-Z) belong to Southeast Asians. (AA) Haplotype network of ACE2 in consolidation of East Asian groups.

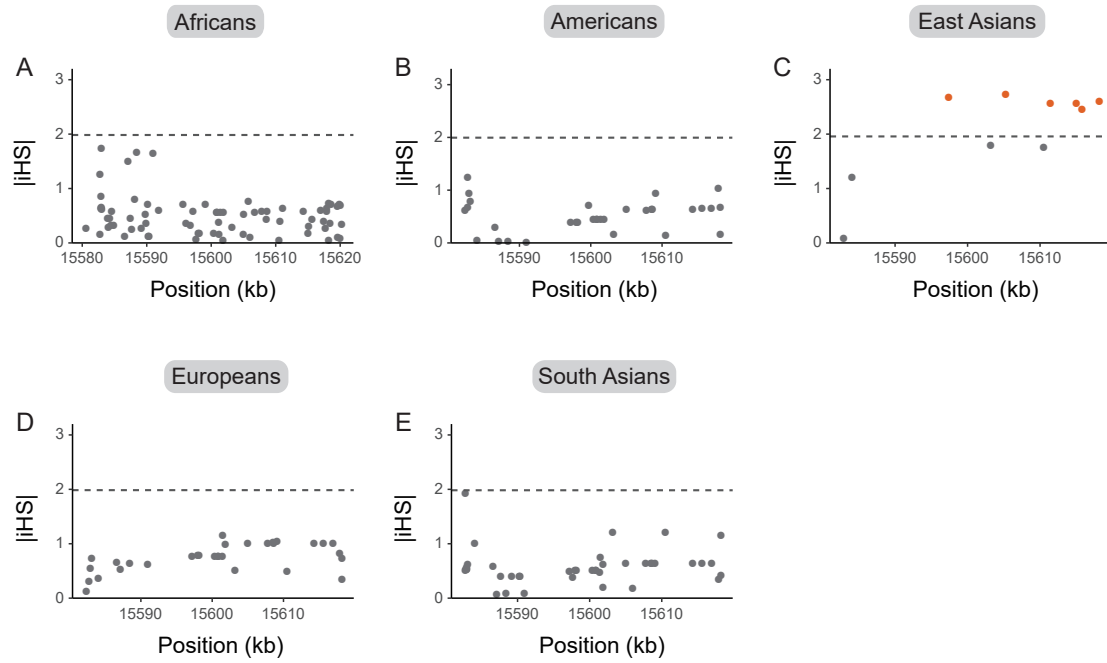


Figure S2. The $|iHS|$ scores of SNPs within the *ACE2* in human populations of five continents. Dotted lines represent the top 5% of $|iHS|$ scores at chromosome X, and outlier SNPs with selection are labeled in orange.